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FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH' ENTERED AT 18:06:24 ON 14 SEP 2004

L1 59302 S ELEGANS
L2 2957 S REVIEW AND L1
L3 21954 S C(W)ELEGANS
L4 457 S PARASITE AND L3
L5 18 S REVIEW AND L4
L6 15 DUP REM L5 (3 DUPLICATES REMOVED)

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L6 ANSWER 1 OF 15 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AU Ullu E (Reprint); Tschudi C; Chakraborty T
TI RNA interference in protozoan **parasites**
SO CELLULAR MICROBIOLOGY, (JUN 2004) Vol. 6, No. 6, pp. 509-519.
Publisher: BLACKWELL PUBLISHING LTD, 9600 GARSINGTON RD, OXFORD OX4 2DG, OXON, ENGLAND.
ISSN: 1462-5814.
AB RNA interference or RNAi is defined as the mechanism through which gene-specific, double-stranded RNA (dsRNA) triggers degradation of homologous transcripts. Besides providing an invaluable tool to downregulate gene expression in a variety of organisms, it is now evident that RNAi extends its tentacles into both the nucleus and the cytoplasm and is involved in a variety of gene silencing phenomena. Here we **review** the current status of RNAi in protozoan **parasites** that cause diseases of considerable medical and veterinary importance throughout Africa, Asia and the Americas. RNAi was first discovered in Trypanosoma brucei, a species of the family Trypanosomatidae, and it rapidly became the method of choice to downregulate gene expression in these organisms. At the same time, mechanistic studies exposed a role for RNAi in the control of retroposon transcript abundance. Whereas RNAi is also present in T. congolense, other members of the same family of organisms, namely T. cruzi and Leishmania major, are RNAi-negative. In apicomplexan **parasites**, there is experimental evidence for RNAi in Plasmodium, but this is not supported by their genetic make up. In contrast, the genome of Toxoplasma gondii harbours gene candidates with convincing similarity to 'classical' RNAi genes. Thus, as previously shown in fungi, protozoan **parasites** are genetically heterogeneous as far as the RNAi pathway is concerned. Finally, database mining predicts that Entamoeba histolytica and Giardia intestinalis have an RNAi pathway and the presence of RNAi genes in Giardia supports the view that gene silencing by dsRNA appeared very early during evolution of the eukaryotic lineage.

L6 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AU Walker, Robert J.; Rogers, Candida M.; Franks, Christopher J.; Holden-Dye, Lindy
TI Electrophysiological and pharmacological studies on excitable tissues in nematodes: nematode electrophysiology and pharmacology
SO Cell Signalling in Prokaryotes and Lower Metazoa (2004), 243-301.
Editor(s): Fairweather, Ian. Publisher: Kluwer Academic Publishers, Dordrecht, Neth.
CODEN: 69FMSE; ISBN: 1-4020-1739-1
AB A **review**. Nematodes include both major **parasites** of humans, livestock, and plants and free-living species such as Caenorhabditis elegans. The nematode nervous system (especially in **C. elegans**) is exceptionally well defined in terms of the number, location and projections of the small number of neurons in the nervous system and their integration into circuits involved in regulatory behaviors vital

to their survival. This chapter will summarize what is known about the biol. activity of neurotransmitters in nematodes: the biosynthetic pathways and genes involved, their receptors, inactivation mechanisms, and second messenger signaling systems. It will cover the classical transmitters, such as acetylcholine (ACh), GABA, glutamate, serotonin, dopamine, octopamine, noradrenaline, and nitric oxide. The localization of peptides throughout the nematode nervous system is summarized, in addition to the isolation of nematode neuropeptides by both traditional biochem. techniques and more modern genetic means. The major contribution of the completion of the **C. elegans** genome-sequencing program is highlighted throughout. Efforts to unravel neurotransmitter action in various physiol. actions such as locomotion, feeding and reproduction are detailed, as well as the various inactivation mechanisms for the current complement of the nematode transmitters.

L6 ANSWER 3 OF 15 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AU Agrawal N; Dasaradhi P V N; Mohmmed A; Malhotra P; Bhatnagar R K; Mukherjee S K (Reprint)

TI RNA interference: Biology, mechanism, and applications

SO MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS, (DEC 2003) Vol. 67, No. 4, pp. 657-+.
Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
ISSN: 1092-2172.

AB RNA silencing is a novel gene regulatory mechanism that limits the transcript level by either suppressing transcription (transcriptional gene silencing [TGS]) or by activating a sequence-specific RNA degradation process (posttranscriptional gene silencing [PTGS]/RNA interference [RNAi]). Although there is a mechanistic connection between TGS and PTGS, TGS is an emerging field while PTGS is undergoing an explosion in its information content. Here, we have limited our discussion to PTGS/RNAi-related phenomena.

Pioneering observations on PTGS/RNAi were reported in plants, but later on RNAi-related events were described in almost all eukaryotic organisms, including protozoa, flies, nematodes, insects, **parasites**, and mouse and human cell lines, as shown in Table 1. Three phenotypically different but mechanistically similar forms of RNAi, cosuppression or PTGS in plants, quelling in fungi, and RNAi in the animal kingdom, have been described. More recently, micro-RNA formation, heterochromatinization, etc., have been revealed as other facets of naturally occurring RNAi processes of eukaryotic cells.

During the occurrence of RNAi/PTGS, double-stranded RNA (dsRNA) molecules, which cleave the inducer molecules into smaller pieces first (16) and eventually destroy the cellular or viral cognate mRNA molecules (called the target) (17) act as inducers or activators of this process. As a result, the target mRNAs cannot accumulate in the cytosol, although they remain detectable by nuclear run-on assays (73). In certain instances, the DNA expressing the target mRNA also undergoes methylation as a by-product of the degradation process (226).

The natural functions of RNAi and its related processes seem to be protection of the genome against invasion by mobile genetic elements such as viruses and transposons as well as orchestrated functioning of the developmental programs of eukaryotic organisms. There are several excellent recent **reviews** which deal with different aspects of RNAi separately (95, 191). Here, we have put together the various aspects of the RNAi process known to date, identified the mechanistic similarities and differences operating in various forms of eukaryotic life, and focused on the experimental results that have led to conceptual advancements in this field.

L6 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN

AU Ikeda, Takanori

TI Pharmacological effects of ivermectin, an antiparasitic agent for

intestinal strongyloidiasis: its mode of action and clinical efficacy
SO Nippon Yakurigaku Zasshi (2003), 122(6), 527-538
CODEN: NYKZAU; ISSN: 0015-5691
AB A **review**. Ivermectin is an oral semi-synthetic lactone anthelmintic agent derived from avermectins isolated from fermentation products of Streptomyces avermitilis. Ivermectin showed a concentration-dependent inhibitory effect on motility of a free-living nematode, Caenorhabditis elegans (**C. elegans**). There exist specific binding sites having a high affinity for ivermectin in the membrane fraction of **C. elegans**, and a strong pos. correlation was detected between the affinity for these binding sites and the suppressive effect on motility of **C. elegans** in several ivermectin-related substances. These results suggested that the binding to these binding sites is important for the nematocidal activity of ivermectin. In oocytes of Xenopus laevis injected with the Poly (A)+ RNA of **C. elegans**, expression of a chloride channel, which is irreversibly activated by ivermectin, was recognized. The pharmacol. properties of this channel suggest that the ivermectin-sensitive channel is a glutamate-activated chloride channel. As to the glutamate-activated chloride channel, two subtypes (GluCl-α and GluCl-β) were cloned, suggesting these subtypes constitute the glutamate-activated chloride channel. These findings suggest that ivermectin binds to glutamate-activated chloride channels existing in nerve or muscle cells of nematode with a specific and high affinity, causing hyperpolarization of nerve or muscle cells by increasing permeability of chloride ion through the cell membrane, and as a result, the **parasites** are paralyzed to death. In exptl. infections in sheep and cattle, ivermectin exhibited potent dose-dependent anthelmintic effects on Haemonchus, Ostertagia, Trichostrongylus, Cooperia, Oesphagostomum, and Dictyocaulus. Anthelmintic effects were reported also in dogs, horses, and humans infected with Strongyloides. In the clin. Phase III trial in Japan, 50 patients infected with Strongyloides stercoralis were administered approx. 200 μg/kg of ivermectin to be given orally twice at an interval of 2 wk. As a result, the Strongyloides stercoralis-eradicating rate was 98.0% (49/50).

L6 ANSWER 5 OF 15 MEDLINE on STN DUPLICATE 1
AU Garofalo Antonio; Kennedy Malcolm W; Bradley Janette E
TI The FAR proteins of parasitic nematodes: their possible involvement in the pathogenesis of infection and the use of Caenorhabditis elegans as a model system to evaluate their function.
SO Medical microbiology and immunology, (2003 Feb) 192 (1) 47-52.
Journal code: 0314524. ISSN: 0300-8584.
AB Parasitic nematodes secrete a structurally novel class of fatty acid and retinol-binding (FAR) protein into the surrounding tissues of the host. These proteins are of interest because they may play an important role in scavenging fatty acids and retinoids from the host that are essential for the survival of the **parasite** and also because the localised depletion of such lipids may have immunomodulatory effects that compromise the host immune response. Research into the biological function(s) of the FAR proteins has been severely hampered by the difficulties associated with the life-cycle propagation of parasitic nematodes and the current intractability of the **parasites** to reverse-genetic studies. The genome of the free-living nematode Caenorhabditis elegans, however, encodes eight FAR-like proteins, and in this **review** we compare the FAR proteins of **C. elegans** and parasitic nematodes, and we discuss the suitability of **C. elegans** as a model system to investigate the biological function(s) of the FAR proteins of parasitic nematodes.

L6 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AU Beall, Melissa J.; Pearce, Edward J.
TI Transforming growth factor-beta and insulin-like signalling pathways in parasitic helminths

SO International Journal for Parasitology (2002), 32(4), 399-404
CODEN: IJPYBT; ISSN: 0020-7519

AB A **review**. The signal transduction pathways involved in regulating developmental arrest in the free-living nematode, Caenorhabditis elegans, are fairly well characterized. However, much less is known about how these processes may influence the developmental timing and maturation in helminth **parasites**. Here, the authors provide an overview of two signaling pathways implicated in the regulation of dauer larva formation in **C. elegans**, the insulin-like signaling pathway and the transforming growth factor-beta pathway, and explore what is known about these signaling pathways in a variety of parasitic helminths. Understanding the differences about how these pathways are affected by environmental cues in free-living vs. parasitic species of helminths may provide insights into novel mechanisms for the control or prevention of helminth-induced disease.

L6 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN

AU Hashmi, Sarwar; Tawe, Wilson; Lustigman, Sara

TI Caenorhabditis elegans and the study of gene function in **parasites**

SO Trends in Parasitology (2001), 17(8), 387-393
CODEN: TPRACT; ISSN: 1471-4922

AB A **review** with refs. The free-living nematode Caenorhabditis elegans is a tractable exptl. model system for the study of both vertebrate and invertebrate biol. Its most significant advantages are its simplicity, both in anatomy and in genomic organization, and the elaborate methods that have been developed to attribute function to previously uncharacterized genes. Importantly, >40% of parasitic nematode genes exhibit high levels of homol. to genes within the **C. elegans** genome. Studying such genes using the **C. elegans** model should yield new insights into key mols. and their possible implications in **parasite** survival, leading to the discovery of new drug targets and vaccine candidates.

L6 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN

AU Geary, Timothy G.; Thompson, David P.

TI Caenorhabditis elegans: how good a model for veterinary **parasites**?

SO Veterinary Parasitology (2001), 101(3-4), 371-386
CODEN: VPARDI; ISSN: 0304-4017

AB A **review**. The organism about which most is known on a mol. level is a nematode, the free-living organism Caenorhabditis elegans. This organism has served as a reasonable model for the discovery of anthelmintic drugs and for research on the mechanism of action of anthelmintics. Useful information on mechanisms of anthelmintic resistance was also obtained from studies on **C. elegans**. Unfortunately, there was not a large-scale extension of genetic techniques developed in **C. elegans** to research on parasitic species of veterinary (or human) **parasites**. Much can be learned about the essentials of nematode biol. by studying **C. elegans**, but discovering the basic biol. of nematode parasitism can only be gained through comparative studies on multiple parasitic species.

L6 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN

AU Dent, Joseph A.

TI What can Caenorhabditis elegans tell us about nematocides and **parasites**?

SO Biotechnology and Bioprocess Engineering (2001), 6(4), 252-263
CODEN: BBEIAU; ISSN: 1226-8372

AB A **review**, with refs. Nematode infections compromise human health and reduce agricultural productivity. Expts. that exploit the powerful mol. genetics of the free-living nematode Caenorhabditis elegans have contributed to the authors' understanding of how the major classes of anthelmintic nematocides kill worms and how worms might evolve resistance

to these drugs. In **C. elegans**, as in **parasites**, benzimidizoles interfere with microtubule polymerization, the imidazothiazoles/tetrahydropyrimidines activate nicotinic acetylcholine receptors, and the macrocyclic lactones activate glutamate-gated chloride channels. Mutant alleles of genes that encode drug targets often confer resistance in **C. elegans**. Preliminary evidence suggests that alleles of homologous genes in **parasites** will, in many cases, also play a role in resistance. Thus, information acquired from **C. elegans** can be usefully applied to understand the mechanisms of drug sensitivity and the genetics of resistance in **parasites**.

L6 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AU Cheeseman, C. L.; Delany, N. S.; Woods, D. J.; Wolstenholme, A. J.
TI High-affinity ivermectin binding to recombinant subunits of the Haemonchus contortus glutamate-gated chloride channel
SO Molecular and Biochemical Parasitology (2001), 114(2), 161-168
CODEN: MBIPDP; ISSN: 0166-6851
AB A **review** with 25 refs. Glutamate-gated chloride channels (GluCls) are targets for the avermectin anthelmintics. A family of five GluCl subunit genes encoding seven subunits has been identified in Caenorhabditis elegans. We have previously shown that two orthologous genes in the **parasite**, Haemonchus contortus, encode three GluCl subunits (HcGluClβ, Hcgbr-2A and Hcgbr-2B) with high amino-acid identity (>80%) to their **C. elegans** counterparts. We amplified and cloned a further subunit cDNA, HcGluClα, from H. contortus eggs. Sequence comparisons suggested that this subunit was closely related to, but not orthologous with, the **C. elegans** GluClα1, α2 or α3/GBR-2 subunits (.apprx.55% amino-acid identity). The HcGluClα cDNA from an ivermectin-resistant isolate contained no coding changes from the wild-type. All of the known H. contortus GluCl cDNA clones were subcloned into the expression vector pcDNA3.1 and transiently expressed in COS-7 cells. As predicted by functional data from the **C. elegans** orthologues, the Hcgbr-2A and HcGluClβ subunits failed to bind [3H]ivermectin. The Hcgbr-2B and HcGluClα subunits bound [3H]ivermectin with high affinity; the Kd values were 70±16 and 26±12 pM, resp. This binding was inhibited by a variety of avermectins, though cold ivermectin was the most potent inhibitor of [3H] ivermectin binding. Picrotoxin, fipronil, glutamate and GABA all failed to compete for ivermectin binding to either subunit. The affinity of [3H]ivermectin binding to H. contortus L3 P2 larval membrane prepns. was re-examined and 70±7 pM. The properties of orthologous GluCl subunits are likely to be conserved across species, but the repertoire and relative importance of those subunits may vary.

L6 ANSWER 11 OF 15 MEDLINE on STN
AU Brownlee D; Holden-Dye L; Walker R
TI The range and biological activity of FMRFamide-related peptides and classical neurotransmitters in nematodes.
SO Advances in parasitology, (2000) 45 109-80. Ref: 260
Journal code: 0370435. ISSN: 0065-308X.
AB Nematodes include both major **parasites** of humans, livestock and plants in addition to free-living species such as Caenorhabditis elegans. The nematode nervous system (especially in **C. elegans**) is exceptionally well defined in terms of the number, location and projections of the small number of neurons in the nervous system and their integration into circuits involved in regulatory behaviours vital to their survival. This **review** will summarize what is known about the biological activity of neurotransmitters in nematodes: the biosynthetic pathways and genes involved, their receptors, inactivation mechanisms and secondary messenger signalling systems. It will cover the 'classical' transmitters, such as acetylcholine (ACh), GABA, glutamate, serotonin, dopamine, octopamine, noradrenaline and nitric oxide. The localization of

peptides throughout the nematode nervous system is summarized, in addition to the isolation of nematode neuropeptides by both traditional biochemical techniques and more modern genetic means. The major contribution of the completion of the **C. elegans** genome-sequencing program is highlighted throughout. Efforts to unravel neurotransmitter action in various physiological actions such as locomotion, feeding and reproduction are detailed as well as the various inactivation mechanisms for the current complement of nematode transmitters.

L6 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AU Bird, David McK; Opperman, Charles H.; Jones, Steven J. M.; Baillie, David L.
TI The Caenorhabditis elegans genome: a guide in the post genomics age
SO Annual Review of Phytopathology (1999), 37, 247-265
CODEN: APPYAG; ISSN: 0066-4286
AB A **review** with 67 refs. The completion of the entire genome sequence of the free-living nematode, Caenorhabditis elegans is a tremendous milestone in modern biol. Not only will scientists be poring over data mined from this resource, but techniques and methodologies developed along the way have changed the way the authors can approach biol. questions. The completion of the **C. elegans** genomic sequence will be of particular importance to scientists working on parasitic nematodes. In many cases, these nematode species present intractable challenges to those interested in their biol. and genetics. The data already compared from **parasites** to the **C. elegans** database reveals a wealth of opportunities for **parasite** biologists. It is likely that many of the same genes will be present in **parasites** and that these genes will have similar functions. Addnl. information regarding differences between free-living and parasitic species will provide insight into the evolution and nature of parasitism. Finally, genetic and genomic approaches to the study of parasitic nematodes now have a clearly marked path to follow.

L6 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AU Brownlee, David J. A.; Fairweather, Ian
TI Exploring the neurotransmitter labyrinth in nematodes
SO Trends in Neurosciences (1999), 22(1), 16-24
CODEN: TNSCDR; ISSN: 0166-2236
AB A **review**, with 86 refs. Nematodes include both free-living species such as Caenorhabditis elegans and major **parasites** of humans, livestock, and plants. The apparent simplicity and uniformity of their nervous system belies a rich diversity of putative signaling mols., particularly neuropeptides. This new appreciation stems largely from the genome-sequencing project with **C. elegans**, which is due to be completed by the end of 1998. The project has provided addnl. insights into other aspects of nematode neurobiol., as have studies on the mechanism of action of anthelmintics. Here, progress on the identification, localization, synthesis, and physiol. actions of transmitters identified in nematodes is explored.

L6 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AU Blaxter, Mark
TI Caenorhabditis elegans is a nematode
SO Science (Washington, D. C.) (1998), 282(5396), 2041-2046
CODEN: SCIEAS; ISSN: 0036-8075
AB A **review** with 46 refs. Caenorhabditis elegans is a rhabditid nematode. What relevance does this have for the interpretation of the complete genome sequence, and how will it affect the exploitation of the sequence for scientific and social ends. Nematodes are only distantly related to humans and other animal groups; will this limit the universality of the **C. elegans** story. Many nematodes are **parasites**; can knowledge of the **C. elegans** sequence aid in the prevention and treatment of disease. This **review** discusses **C. elegans** place in the tree

of life, other nematode species, nematode-specific genes, and comparative nematode genomics.

L6 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AU Bird, D. McK.; Opperman, C. H.
TI Caenorhabditis elegans: a genetic guide to parasitic nematode biology
SO Journal of Nematology (1998), 30(3), 299-308
CODEN: JONEB5; ISSN: 0022-300X
AB A **review**, with 37 refs. The advent of **parasite** genome sequencing projects, as well as an increase in biol.-directed gene discovery, promises to reveal genes encoding many of the key mols. required for nematode-host interactions. However, distinguishing parasitism genes from those merely required for nematode viability remains a substantial challenge. Although this will ultimately require a functional test in the host or **parasite**, the free-living nematode **C. elegans** can be exploited as a heterologous system to determine function of candidate parasitism genes. Studies of **C. elegans** also have revealed genetic networks, such as the dauer pathway, that may also be important adaptations for parasitism. As a more directed means of identifying parasitism traits, we developed classical genetics for Heterodera glycines and have used this approach to map genes conferring host resistance-breaking phenotypes. It is likely that the **C. elegans** and H. glycines genomes will be at least partially syntenic, thus permitting predictive phys. mapping of H. glycines genes of interest.

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Terms	Documents
L2 and L5	12

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US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

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L5	transgen$ near10 l1	36	L5
L4	l1 and l2	2530	L4
L3	l1 with L2	3	L3
L2	bombard$ or microprojectile	41964	L2
L1	schistosome or parasite	18104	L1

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Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. 6759390. 02 Mar 01; 06 Jul 04. Compounds and their uses. Martin-Lomas; Manuel, et al. 514/25; 536/17.2 536/18.4 536/4.1. A61K031/70 C07H017/00 C07H015/00.

☐ 2. 6716826. 02 Mar 01; 06 Apr 04. Compounds and their uses. Martin-Lomas; Manuel, et al. 514/54; 514/25 514/35 514/53 514/62 514/866 536/17.2. A61K031/715 A61K031/70.

☐ 3. 3943453. 20 Feb 74; 09 Mar 76. High voltage rapid switching circuit. Melchior; Gerald. 327/365; 327/374. H03K017/00 G11C011/26.

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L1 with L2	3

Prev Page Next Page Go to Doc#

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Search Results - Record(s) 1 through 12 of 12 returned.

☐ 1. 20040172671. 22 Jan 04. 02 Sep 04. Transgenic plants protected against parasitic plants. Ali, Radi, et al. 800/278; 800/279 A01H001/00 C12N015/82.

☐ 2. 20040081958. 06 Jun 01. 29 Apr 04. Identification and use of molecular markers indicating cellular reprogramming. Eilertsen, Ken, et al. 435/6; 536/23.1 702/20 C12Q001/68 G06F019/00 G01N033/48 G01N033/50 C07H021/04.

☐ 3. 20030217378. 02 Apr 03. 20 Nov 03. Cloning using rapidly matured oocytes. Stice, Steven L., et al. 800/15; 800/17 800/21 A01K067/027.

☐ 4. 20030204869. 11 Apr 02. 30 Oct 03. Method to control the ripening of papaya fruit and confer disease resistance to papaya plants. Gonsalves, Dennis, et al. 800/280; 536/23.6 800/287 800/295 A01H005/00 C07H021/04 C12N015/82.

☐ 5. 20030181376. 31 Mar 03. 25 Sep 03. Control of crop pests & animal parasites through direct neuronal uptake. Atkinson, Howard John, et al. 514/12; A01N065/00.

☐ 6. 20030172397. 11 Apr 02. 11 Sep 03. Papaya ringspot virus genes. Gonsalves, Dennis, et al. 800/280; 435/320.1 435/419 536/23.72 800/295 A01H005/00 C07H021/04 C12N015/82 C12N005/04.

☐ 7. 20030166282. 31 Jan 03. 04 Sep 03. High potency siRNAS for reducing the expression of target genes. Brown, David, et al. 435/455; 435/375 C12N005/02 C12N015/85.

☐ 8. 20020094555. 21 Apr 00. 18 Jul 02. Locked nucleic acid hybrids and methods of use. Belotserkovskii, Boris P., et al. 435/183; 530/350 536/23.1 C07K017/00 C07H021/02 A61K031/70 C12N009/00.

☐ 9. 20020064859. 13 Jul 01. 30 May 02. Adenovirus vectors comprising introns. Tikoo, Suresh K.. 435/235.1; 424/199.1 435/320.1 A61K039/12 C12N015/861 C12N007/01.

☐ 10. 20020013957. 28 Dec 00. 31 Jan 02. Method of cloning porcine animals. Damiani, Philip, et al. 800/24; 800/17 A01K067/027.

☐ 11. 6700037. 28 Dec 00; 02 Mar 04. Method of cloning porcine animals. Damiani; Philip, et al. 800/24; 800/17 800/8. A12N015/00 A01K067/00 A01K067/027.

☐ 12. 6258998. 24 Nov 98; 10 Jul 01. Method of cloning porcine animals. Damiani; Philip, et al. 800/24; 800/17 800/8. C12N015/00 A01K067/00 A01K067/027.

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